G1000PCT.ST25
SEQUENCE LISTING

<110> Gesellschaft für Biotechnologische Forschung mbH

Ferrer, Manuel

Chernikova, Tatjana

Golyshin, Peter

Timmis, Kenneth

Yakimov, Michail

<120> Transgenic organisms with lower growth temperatures

<130> G1000PCT

<150> EP 03023032.0

<151> 2003-10-13

<160> 28

<170> PatentIn version 3.1

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<211> 97

<212> PRT

<213> artificial sequence

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<223> Cpn10

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            20   25   30

Glu Lys Pro Asn Gln Gly Val Val Ile Ser Val Gly Thr Gly Arg Ile
        35   40   45

Leu Asp Asn Gly Ser Val Gln Ala Leu Ala Val Asn Glu Gly Asp Val

          50   55   60

Val Val Phe Gly Lys Tyr Ser Gly Gln Asn Thr Ile Asp Ile Asp Gly
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Pro Lys Gly Arg Asn Val Val Ile Glu Lys Ser Phe Gly Ala Pro Ile
            35   40   45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Lys Asp
        50   55   60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Gln
65   70   75   80

Ala Asn Asp Gln Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
                85   90   95

Gln Ala Ile Ile Ser Glu Gly Leu Lys Ser Val Ala Ala Gly Met Asn
                100   105   110

Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Thr Ala Ala Val Val
            115   120   125

Ala Ala Ile Lys Glu Gln Ala Gln Pro Cys Leu Asp Thr Lys Ala Ile
        130   135   140

Ala Gln Val Gly Thr Ile Ser Ala Asn Ala Asp Glu Thr Val Gly Arg
145   150   155   160

Leu Ile Ala Glu Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr
                    165   170   175

Val Glu Glu Gly Lys Gly Leu Glu Asp Glu Leu Asp Val Val Glu Gly
              180   185   190

Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Asn Gln
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Glu Lys Met Thr Val Glu Met Glu Asn Pro Leu Ile Leu Leu Val Asp
     210   215   220

Lys Lys Ile Asp Asn Leu Gln Glu Leu Leu Pro Ile Leu Glu Asn Val
225   230   235   240

Ala Lys Ser Gly Arg Pro Leu Leu Ile Val Ala Glu Asp Val Glu Gly
              245   250   255

Gln Ala Leu Ala Thr Leu Val Val Asn Asn Leu Arg Gly Thr Phe Lys
         260   265   270

Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
     275   280   285

Leu Gln Asp Leu Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu
     290   295   300

Leu Gly Met Ser Leu Glu Thr Ala Asp Pro Ser Ser Leu Gly Thr Ala
305   310   315   320

Ser Lys Val Val Ile Asp Lys Glu Asn Thr Val Ile Val Asp Gly Ala
              325   330   335

Gly Thr Glu Ala Ser Val Asn Thr Arg Val Asp Gln Ile Arg Ala Glu
         340   345   350

Ile Glu Ser Ser Thr Ser Asp Tyr Asp Ile Glu Lys Leu Gln Glu Arg
         355   360   365

Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Gly
     370   375   380

Ser Glu Met Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu
385   390   395   400

His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
              405   410   415

Val Ala Leu Ile Arg Ala Leu Ser Ser Val Thr Val Val Gly Asp Asn
         420   425   430

Seite 3

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Glu Asp Gln Asn Val Gly Ile Ala Leu Ala Leu Arg Ala Met Glu Ala
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Pro Ile Arg Gln Ile Ala Gly Asn Ala Gly Ala Glu Gly Ser Val Val
        450             455             460

Val Asp Lys Val Lys Ser Gly Thr Gly Ser Phe Gly Phe Asn Ala Ser
465             470             475             480

Thr Gly Glu Tyr Gly Asp Met Ile Ala Met Gly Ile Leu Asp Pro Ala
                485             490             495

Lys Val Thr Arg Ser Ser Leu Gln Ala Ala Ala Ser Ile Ala Gly Leu
            500             505             510

Met Ile Thr Thr Glu Ala Met Val Ala Asp Ala Pro Val Glu Glu Gly
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            20                  25                  30

Thr Thr Gln Gln Asp Asn Leu Tyr Thr Gly Val Met Ser Leu Ala Arg
            35                  40                  45

Asp Ser Ala Gly Leu Glu Val Lys Thr Ala Ser Ala Gly Asp Val Asn
        50                  55                  60

Leu Thr Tyr Met Glu Arg Gln Gly Ser Asp Lys Asp Asn Ala Glu Ser
65                  70                  75                  80

Val Ile Leu Leu His Gly Phe Ser Ala Asp Lys Asp Asn Trp Ile Leu
                85                  90                  95

Phe Thr Lys Glu Phe Asp Glu Lys Tyr His Val Ile Ala Val Asp Leu
            100                 105                 110

Ala Gly His Gly Asp Ser Glu Gln Leu Leu Thr Thr Asp Tyr Gly Leu
            115                 120                 125

Ile Lys Gln Ala Glu Arg Leu Asp Ile Phe Leu Ser Gly Leu Gly Val
        130                 135                 140

Asn Ser Phe His Ile Ala Gly Asn Ser Met Gly Gly Ala Ile Ser Ala
145                 150                 155                 160

Ile Tyr Ser Leu Ser His Pro Glu Lys Val Lys Ser Leu Thr Leu Ile
                165                 170                 175

Asp Ala Ala Gly Val Asp Gly Asp Thr Glu Ser Glu Tyr Tyr Lys Val
            180                 185                 190

Leu Ala Glu Gly Lys Asn Pro Leu Ile Ala Thr Asp Glu Ala Ser Phe
            195                 200                 205

Glu Tyr Arg Met Gly Phe Thr Met Thr Gln Pro Pro Phe Leu Pro Trp
210                 215                 220
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Pro Leu Arg Pro Ser Leu Leu Arg Lys Thr Leu Ala Arg Ala Glu Ile
225   230   235   240

Asn Asn Lys Ile Phe Ser Asp Met Leu Lys Thr Lys Glu Arg Leu Gly
            245   250   255

Met Thr Asn Phe Gln Gln Lys Ile Glu Val Lys Met Ala Gln His Pro
            260   265   270

Leu Pro Thr Leu Ile Met Trp Gly Lys Glu Asp Arg Val Leu Asp Val
            275   280   285

Ser Ala Ala Ala Ala Phe Lys Lys Ile Ile Pro Gln Ala Thr Val His
        290   295   300

Ile Phe Pro Glu Val Gly His Leu Pro Met Val Glu Ile Pro Ser Glu
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Ser Ala Lys Val Tyr Glu Glu Phe Leu Ser Ser Ile Lys
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<213> artificial sequence

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<223> cpn10

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Glu Lys Pro Asn Gln Gly Val Val Ile Ser Val Gly Thr Gly Arg Ile
        35                  40                  45


Leu Asp Asn Gly Ser Val Gln Ala Leu Ala Val Asn Glu Gly Asp Val
    50                  55                  60
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Val Val Phe Gly Lys Tyr Ser Gly Gln Asn Thr Ile Asp Ile Asp Gly
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                20   25   30

Pro Lys Gly Arg Asn Val Val Ile Glu Lys Ser Phe Gly Ala Pro Ile
        35   40   45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Lys Asp
        50   55   60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Gln
65   70   75   80

Ala Asn Asp Gln Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
                85   90   95

Gln Ala Ile Ile Ser Glu Gly Leu Lys Ser Val Ala Ala Gly Met Asn
                100   105   110

Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Thr Ala Ala Val Val
            115   120   125

Ala Ala Ile Lys Glu Gln Ala Gln Pro Cys Leu Asp Thr Lys Ala Ile
        130   135   140

Ala Gln Val Gly Thr Ile Ser Ala Asn Ala Asp Glu Thr Val Gly Arg
145   150   155   160

Leu Ile Ala Glu Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr
              165   170   175

Val Glu Glu Gly Lys Gly Leu Glu Asp Glu Leu Asp Val Val Glu Gly
              180   185   190

Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Asn Gln
              195   200   205

Glu Lys Met Thr Val Glu Met Glu Asn Pro Leu Ile Leu Leu Val Asp
    210   215   220

Lys Lys Ile Asp Asn Leu Gln Glu Leu Leu Pro Ile Leu Glu Asn Val
225   230   235   240

Ala Lys Ser Gly Arg Pro Leu Leu Ile Val Ala Glu Asp Val Glu Gly
              245   250   255

Gln Ala Leu Ala Thr Leu Val Val Asn Asn Leu Arg Gly Thr Phe Lys
              260   265   270

Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
              275   280   285

Leu Gln Asp Leu Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu
    290   295   300

Leu Gly Met Ser Leu Glu Thr Ala Asp Pro Ser Ser Leu Gly Thr Ala
305   310   315   320

Ser Lys Val Val Ile Asp Lys Glu Asn Thr Val Ile Val Asp Gly Ala
              325   330   335

Gly Thr Glu Ala Ser Val Asn Thr Arg Val Asp Gln Ile Arg Ala Glu
              340   345   350

Ile Glu Ser Ser Thr Ser Asp Tyr Asp Ile Glu Lys Leu Gln Glu Arg
              355   360   365

Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Gly
    370   375   380

Ser Glu Met Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu
385   390   395   400

His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
              405   410   415

Val Ala Leu Ile Arg Ala Leu Ser Ser Val Thr Val Val Gly Asp Asn
              420   425   430

Seite 11

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Glu Asp Gln Asn Val Gly Ile Ala Leu Ala Leu Arg Ala Met Glu Ala
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Pro Ile Arg Gln Ile Ala Gly Asn Ala Gly Ala Glu Gly Ser Val Val
        450             455             460

Val Asp Lys Val Lys Ser Gly Thr Gly Ser Phe Gly Phe Asn Ala Ser
465             470             475             · 480

Thr Gly Glu Tyr Gly Asp Met Ile Ala Met Gly Ile Leu Asp Pro Ala
            485             490             495

Lys Val Thr Arg Ser Ser Leu Gln Ala Ala Ala Ser Ile Ala Gly Leu
        500             505             510

Met Ile Thr Thr Glu Ala Met Val Ala Asp Ala Pro Val Glu Glu Gly
        515             520             525

Ala Gly Gly Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met
        530             535             540

Pro Gly Met Met
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<210> 8

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<213> Oleispira antarctica

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            20              25              30

Thr Thr Gln Gln Asp Asn Leu Tyr Thr Gly Val Met Ser Leu Ala Arg
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Asp Ser Ala Gly Leu Glu Val Lys Thr Ala Ser Ala Gly Asp Val Asn
        50              55              60

Leu Thr Tyr Met Glu Arg Gln Gly Ser Asp Lys Asp Asn Ala Glu Ser
65              70              75              80

Val Ile Leu Leu His Gly Phe Ser Ala Asp Lys Asp Asn Trp Ile Leu
            85              90              95

Phe Thr Lys Glu Phe Asp Glu Lys Tyr His Val Ile Ala Val Asp Leu
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                100   105   110

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            130   135   140

    Asn Ser Phe His Ile Ala Gly Asn Ser Met Gly Gly Ala Ile Ser Ala
    145   150   155   160

    Ile Tyr Ser Leu Ser His Pro Glu Lys Val Lys Ser Leu Thr Leu Ile
                165   170   175

    Asp Ala Ala Gly Val Asp Gly Asp Thr Glu Ser Glu Tyr Tyr Lys Val
                180   185   190

    Leu Ala Glu Gly Lys Asn Pro Leu Ile Ala Thr Asp Glu Ala Ser Phe
                195   200   205

    Glu Tyr Arg Met Gly Phe Thr Met Thr Gln Pro Pro Phe Leu Pro Trp
            210   215   220

    Pro Leu Arg Pro Ser Leu Leu Arg Lys Thr Leu Ala Arg Ala Glu Ile
    225   230   235   240

    Asn Asn Lys Ile Phe Ser Asp Met Leu Lys Thr Lys Glu Arg Leu Gly
                245   250   255

    Met Thr Asn Phe Gln Gln Lys Ile Glu Val Lys Met Ala Gln His Pro
                260   265   270

    Leu Pro Thr Leu Ile Met Trp Gly Lys Glu Asp Arg Val Leu Asp Val
            275   280   285

    Ser Ala Ala Ala Ala Phe Lys Lys Ile Ile Pro Gln Ala Thr Val His
        290   295   300

    Ile Phe Pro Glu Val Gly His Leu Pro Met Val Glu Ile Pro Ser Glu
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<210> 9

<211> 5373

<212> DNA

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Glu Lys Pro Asn Gln Gly Val Val Ile Ser Val Gly Thr Gly Arg Ile
        35   40   45

Leu Asp Asn Gly Ser Val Gln Ala Leu Ala Val Asn Glu Gly Asp Val
        50   55   60

Val Val Phe Gly Lys Tyr Ser Gly Gln Asn Thr Ile Asp Ile Asp Gly
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Ala

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<213> artificial sequence

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<223> mutant protein

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Pro Lys Gly Arg Asn Val Val Ile Glu Lys Ser Phe Gly Ala Pro Ile
        35   40   45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Lys Asp
        50   55   60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Gln
65   70   75   80

Ala Asn Asp Gln Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
                85   90   95

Gln Ala Ile Ile Ser Glu Gly Leu Lys Ser Val Ala Ala Gly Met Asn
                100   105   110

Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Thr Ala Ala Val Val

                    115   120   125

Ala Ala Ile Lys Glu Gln Ala Gln Pro Cys Leu Asp Thr Lys Ala Ile
        130   135   140

Ala Gln Val Gly Thr Ile Ser Ala Asn Ala Asp Glu Thr Val Gly Arg
145   150   155   160

Leu Ile Ala Glu Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr
                165   170   175

Val Glu Glu Gly Lys Gly Leu Glu Asp Glu Leu Asp Val Val Glu Gly
            180   185   190

Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Asn Gln
            195   200   205

Glu Lys Met Thr Val Glu Met Glu Asn Pro Leu Ile Leu Leu Val Asp
    210   215   220

Lys Lys Ile Asp Asn Leu Gln Glu Leu Leu Pro Ile Leu Glu Asn Val
225   230   235   240

Ala Lys Ser Gly Arg Pro Leu Leu Ile Val Ala Glu Asp Val Glu Gly
            245   250   255

Gln Ala Leu Ala Thr Leu Val Val Asn Asn Leu Arg Gly Thr Phe Lys
            260   265   270

Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
        275   280   285

Leu Gln Asp Leu Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu
    290   295   300

Leu Gly Met Ser Leu Glu Thr Ala Asp Pro Ser Ser Leu Gly Thr Ala
305   310   315   320

Ser Lys Val Val Ile Asp Lys Glu Asn Thr Val Ile Val Asp Gly Ala
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Gly Thr Glu Ala Ser Val Asn Thr Arg Val Asp Gln Ile Arg Ala Glu
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Ile Glu Ser Ser Thr Ser Asp Tyr Asp Ile Glu Lys Leu Gln Glu Arg
        355   360   365

Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Gly
    370   375   380

Ser Glu Met Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu
385   390   395   400

His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
                    405   410   415

Val Ala Leu Ile Arg Ala Leu Ser Ser Val Thr Val Val Gly Asp Asn
                420   425   430

Glu Asp Gln Asn Val Gly Ile Ala Leu Ala Leu Arg Ala Met Glu Ala
            435   440   445

Pro Ile Arg Gln Ile Ala Gly Asn Ala Gly Ala Ala Gly Ala Ala Val
    450   455   460

Val Asp Lys Val Lys Ser Gly Thr Gly Ser Phe Gly Phe Asn Ala Ser
465   470   475   480

Thr Gly Glu Tyr Gly Asp Met Ile Ala Met Gly Ile Leu Asp Pro Ala
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Lys Val Thr Arg Ser Ser Leu Gln Ala Ala Ala Ser Ile Ala Gly Leu
            500   505   510

Met Ile Thr Thr Glu Ala Met Val Ala Asp Ala Pro Val Glu Glu Gly
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Thr Thr Gln Gln Asp Asn Leu Tyr Thr Gly Val Met Ser Leu Ala Arg
            35   40   45

Asp Ser Ala Gly Leu Glu Val Lys Thr Ala Ser Ala Gly Asp Val Asn
    50   55   60

Leu Thr Tyr Met Glu Arg Gln Gly Ser Asp Lys Asp Asn Ala Glu Ser
65   70   75   80

Val Ile Leu Leu His Gly Phe Ser Ala Asp Lys Asp Asn Trp Ile Leu
            85   90   95

Phe Thr Lys Glu Phe Asp Glu Lys Tyr His Val Ile Ala Val Asp Leu
            100   105   110

Ala Gly His Gly Asp Ser Glu Gln Leu Leu Thr Thr Asp Tyr Gly Leu
            115   120   125

Ile Lys Gln Ala Glu Arg Leu Asp Ile Phe Leu Ser Gly Leu Gly Val
        130   135   140

Asn Ser Phe His Ile Ala Gly Asn Ser Met Gly Gly Ala Ile Ser Ala
145   150   155   160

Ile Tyr Ser Leu Ser His Pro Glu Lys Val Lys Ser Leu Thr Leu Ile
            165   170   175

Asp Ala Ala Gly Val Asp Gly Asp Thr Glu Ser Glu Tyr Tyr Lys Val
            180   185   190

Leu Ala Glu Gly Lys Asn Pro Leu Ile Ala Thr Asp Glu Ala Ser Phe
        195   200   205

Glu Tyr Arg Met Gly Phe Thr Met Thr Gln Pro Pro Phe Leu Pro Trp
    210   215   220

Pro Leu Arg Pro Ser Leu Leu Arg Lys Thr Leu Ala Arg Ala Glu Ile
225   230   235   240

Asn Asn Lys Ile Phe Ser Asp Met Leu Lys Thr Lys Glu Arg Leu Gly
            245   250   255

Met Thr Asn Phe Gln Gln Lys Ile Glu Val Lys Met Ala Gln His Pro
            260   265   270

Leu Pro Thr Leu Ile Met Trp Gly Lys Glu Asp Arg Val Leu Asp Val
        275   280   285

Ser Ala Ala Ala Ala Phe Lys Lys Ile Ile Pro Gln Ala Thr Val His
    290   295   300

Ile Phe Pro Glu Val Gly His Leu Pro Met Val Glu Ile Pro Ser Glu
305   310   315   320

Ser Ala Lys Val Tyr Glu Glu Phe Leu Ser Ser Ile Lys
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<211> 97

<212> PRT

<213> artificial sequence

<220>

<223> Cpn10, nucleotides 458 - 751

<400> 14

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Glu Glu Thr Ala Thr Ala Gly Gly Ile Ile Leu Pro Gly Ala Ala Ala
            20   25   30

Glu Lys Pro Asn Gln Gly Val Val Ile Ser Val Gly Thr Gly Arg Ile
        35   40   45

Leu Asp Asn Gly Ser Val Gln Ala Leu Ala Val Asn Glu Gly Asp Val
    50   55   60

Val Val Phe Gly Lys Tyr Ser Gly Gln Asn Thr Ile Asp Ile Asp Gly
65   70   75   80

Glu Glu Leu Leu Ile Leu Asn Glu Ser Asp Ile Tyr Gly Val Leu Glu
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Ala

<210> 15

<211> 548

<212> PRT

<213> artificial sequence

<220>

<223> Cpn60, nucleotides 458 - 751

<400> 15

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            20   25   30

Pro Lys Gly Arg Asn Val Val Ile Glu Lys Ser Phe Gly Ala Pro Ile
        35   40   45

Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Lys Asp
    50   55   60

Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Gln
65   70   75   80

Ala Asn Asp Gln Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
          85   90   95

Gln Ala Ile Ile Ser Glu Gly Leu Lys Ser Val Ala Ala Gly Met Asn
         100   105   110

Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Thr Ala Ala Val Val
         115   120   125

Ala Ala Ile Lys Glu Gln Ala Gln Pro Cys Leu Asp Thr Lys Ala Ile
     130   135   140

Ala Gln Val Gly Thr Ile Ser Ala Asn Ala Asp Glu Thr Val Gly Arg
145   150   155   160

Leu Ile Ala Glu Ala Met Glu Lys Val Gly Lys Glu Gly Val Ile Thr
             165   170   175

Val Glu Glu Gly Lys Gly Leu Glu Asp Glu Leu Asp Val Val Glu Gly
             180   185   190

Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Asn Gln
         195   200   205

Glu Lys Met Thr Val Glu Met Glu Asn Pro Leu Ile Leu Leu Val Asp
     210   215   220

Lys Lys Ile Asp Asn Leu Gln Glu Leu Leu Pro Ile Leu Glu Asn Val
225   230   235   240

Ala Lys Ser Gly Arg Pro Leu Leu Ile Val Ala Glu Asp Val Glu Gly
             245   250   255

Gln Ala Leu Ala Thr Leu Val Val Asn Asn Leu Arg Gly Thr Phe Lys
         260   265   270

Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
         275   280   285

Leu Gln Asp Leu Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu
     290   295   300

Leu Gly Met Ser Leu Glu Thr Ala Asp Pro Ser Ser Leu Gly Thr Ala
305   310   315   320

Ser Lys Val Val Ile Asp Lys Glu Asn Thr Val Ile Val Asp Gly Ala
             325   330   335

Gly Thr Glu Ala Ser Val Asn Thr Arg Val Asp Gln Ile Arg Ala Glu
         340   345   350

Ile Glu Ser Ser Thr Ser Asp Tyr Asp Ile Glu Lys Leu Gln Glu Arg

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            355                    360                    365
Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Gly
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Ser Glu Met Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu
385                 390                 395                 400

His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
                405                 410                 415

Val Ala Leu Ile Arg Ala Leu Ser Ser Val Thr Val Val Gly Asp Asn
            420                 425                 430

Glu Asp Gln Asn Val Gly Ile Ala Leu Ala Leu Arg Ala Met Glu Ala
        435                 440                 445

Pro Ile Arg Gln Ile Ala Gly Asn Ala Gly Ala Ala Gly Ala Ala Val
    450                 455                 460

Val Asp Lys Val Lys Ser Gly Thr Gly Ser Phe Gly Phe Asn Ala Ser
465                 470                 475                 480

Thr Gly Glu Tyr Gly Asp Met Ile Ala Met Gly Ile Leu Asp Pro Ala
                485                 490                 495

Lys Val Thr Arg Ser Ser Leu Gln Ala Ala Ala Ser Ile Ala Gly Leu
            500                 505                 510

Met Ile Thr Thr Glu Ala Met Val Ala Asp Ala Pro Val Glu Glu Gly
        515                 520                 525

Ala Gly Gly Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met
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Pro Gly Met Met
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<210> 16

<211> 2783

<212> DNA

<213> artificial sequence

<220>

<223> mutant protein

<400> 16

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aagtgatatc tacggcgttt tagaagctta attattacac tcactttttt atttaaccta    780

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actagcacag gcgattatca gcgaaggctt gaaatctgtt gcggctggca tgaatccaat   1140

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ccctgcaaaa gtcacgcgtt catctctaca agccgcggcg tctatcgcag gtttgatgat  2340

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<210> 17

<211> 22

<212> DNA

<213> artificial sequence

<220>

<223> Forward Primer

<220>

<221> misc_feature

<222> (1)..(22)

<223> "n" defines inosine

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<210> 18

<211> 23

<212> DNA

<213> artificial sequence

<220>

<223> Reverse Primer

<220>

<221> misc_feature

<222> (1)..(23)

<223> residue "n" designates inosine

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<210> 19

<211> 13

<212> PRT

<213> Oleispira antarctica

<400> 19

Ser Val Ala Ala Gly Met Asn Pro Met Asp Leu Gln Arg
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<210> 20

<211> 16

<212> PRT

<213> Oleispira antarctica

<400> 20

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<210> 21

<211> 42

<212> DNA

<213> artificial sequence

<220>

<223> Oligonucleotide

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<210> 22

<211> 37

<212> DNA

<213> artificial sequence

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<223> Oligonucleotide

<400> 22
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<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> Oligonucleotide

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<210> 24

<211> 30

<212> DNA

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<223> Oligonucleotide

<400> 24
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<211> 46

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<211>   42

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